

FIGURE 1

CTGTCTGCCCATCTGAATAACAAGAGATGGGGCTTGTGATTTTCTCCACGGTTCTGGGT
 1 -----+-----+-----+-----+-----+ 60
 GACAGACGGGTAGACTTATTGTTCTCTACCCGAACACTAAAGGAGGTGCCAAGACCCA

C M G L V I F L H G S G S -

CTGGTAATGAAGTCATAGAAGGCCCCCAGAATGCAACAGTCCTGAAGGGCTCCCAGGCTC
 61 -----+-----+-----+-----+-----+ 120
 GACCATTACTTCAGTATCTTCCGGGGTCTTACGTTGTCAGGACTTCCCAGGGTCCGAG

C G N E V I E G P Q N A T V L K G S Q A R -

GCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGG
 121 -----+-----+-----+-----+-----+ 180
 CGAAGTTGACGTGGCAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGTACC

C F N C T V S Q G W K L I M W A L S D M V -

TGGTGCTAAGCGTCAGGCCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCTCAGA
 181 -----+-----+-----+-----+-----+ 240
 ACCACGATTTCGAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCGAAGTGGAGAGTCT

C V L S V R P M E P I I T N D R F T S Q R -

GGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTG
 241 -----+-----+-----+-----+-----+ 300
 CCATGCTGGTCCCGCCCTTGAAGTGGAGCCTCTACTAGTAGGTGTTACACCTCGGGTCAC

C Y D Q G G N F T S E M I I H N V E P S D -

ATTGCGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTA
 301 -----+-----+-----+-----+-----+ 360
 TAAGCCCCTTGTAGTCTACGTCGGAGGTCTTGTGTCAGCGGACGTACCTAGACGAATGGAAT

C S G N I R C S L Q N S R L H G S A Y L T -

CCGTCCAAGTTATGGGAGAGCTGTTTATTCCAGTGTTAATCTTGTAGTCGCTGAGAATG
 361 -----+-----+-----+-----+-----+ 420
 GGCAGGTTCAATACCCTCTCGACAAGTAAGGGTCACAATTAGAACATCAGCGACTCTTAC

C V Q V M G E L F I P S V N L V V A E N E -

AACCTTGTGAAGTTACTTGTCTACCCTCACACTGGACCCGGCTCCCGGATATTTCTGGG
 421 -----+-----+-----+-----+-----+ 480
 TTGGAACACTTCAATGAACAGATGGGAGTGTGACCTGGGCCGAGGGCCTATAAAGGACCC

C P C E V T C L P S H W T R L P D I S W E -

AGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTGTTCCGGAGCCCAGCGACCTTC
 481 -----+-----+-----+-----+-----+ 540
 TCGAGCCAGAGGACCAGTCGGTAAGTTCGATAATAAAACAAGGCCTCGGGTCGCTGGAAG

C L G L L V S H S S Y Y F V P E P S D L Q -

AAAGTGCAGTGAGCATCCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTGCGTGG
 541 -----+-----+-----+-----+-----+ 600
 TTTCACGTCACTCGTAGGACCGAGACTGGGGTGTCTCGTTACCCTGAACTGAACGCACC

C S A V S I L A L T P Q S N G T L T C V A -

FIGURE 1 (con't)

601 CTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTCCGGT
 -----+-----+-----+-----+-----+ 660
 GATGGACCTTCTCGGACTTCCGGGCGTTTCCAGACGTTGACATTTAGAGTGACACTAAGCCA
 C T W K S L K A R K S A T V N L T V I R C -
 661 GTCCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTT
 -----+-----+-----+-----+-----+ 720
 CAGGGGTTCTGTGACCTCCACCATAATTATAAGGTCCACATAATAGTTCAAATGGCTCAA
 C P Q D T G G G I N I P G V L S S L P S L -
 721 TAGGTTTTTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTC
 -----+-----+-----+-----+-----+ 780
 ATCCAAAAGTAACGGATGAACCCGTTTCAACCTGAACCTGATCGTCCGTTGGTACGAAG
 C G F S L P T W G K V G L G L A G T M L L -
 781 TGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCT
 -----+-----+-----+-----+-----+ 840
 ACTGCGGCTGCACATGAGAATGTTATGCGACGACGACGACGGCGGCAGCAACAACACCGA
 C T P T C T L T I R C C C C R R R C C G C -
 841 GCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAGAAAAAGAGGATTTTCGTATTCAAT
 -----+-----+-----+-----+-----+ 900
 CGTTGACGACGACGGCAACAACAAGACGACATCTTCTTTTCTCCTAAAGCATAAGTTA
 C N C C C R C C F C C R R K R G F R I Q F -
 901 TTCAAAAGAAATCTGAAAAAGAGAAGACAAACAAAGAACTGAGACAGAAAGTGAAATG
 -----+-----+-----+-----+-----+ 960
 AAGTTTTCTTTAGACTTTTCTCTTCTGTTTGTGTTTCTTTGACTCTGTCTTTCACCTTTAC
 C Q K K S E K E K T N K E T E T E S G N E -
 961 AAAACTCCGGCTACAATTCAGATGAACAAAAGACCACAGACACCGCTTCTCTCCCTCCCA
 -----+-----+-----+-----+-----+ 1020
 TTTTGAGGCCGATGTTAAGTCTACTTGTGTTTCTGGTGTCTGTGGCGAAGAGAGGGAGGGT
 C N S G Y N S D E Q K T T D T A S L P P K -
 1021 AATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCAGC
 -----+-----+-----+-----+-----+ 1080
 TTAGGACACTTAGGTCACTAGGACTTGTGTTTCTTTGTCATCGACACCGGGAGGAGTGGTCG
 C S C E S S D P E Q R N S S C G P P H Q R -
 1081 GGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCA
 -----+-----+-----+-----+-----+ 1140
 CCCGACTAGTTGCAGGTGGGTCCGGTTCAGTAGGTGTCCGAAGAAAATTAGACCGGT
 C A D Q R P P R P A S H P Q A S F N L A S -
 1141 GTCCTGAGAAGGTCAGTAATACAACCTGTAGTATAG
 -----+-----+-----+-----+ 1175
 CAGGACTCTTCCAGTCATTATGTTGACATCATATC
 C P E K V S N T T V V * -

FIGURE 2

1 AGTGATCATGGTGGCAGGAGCCATGGAAAATAGAGACCCACCCGGTCTGGGTCTGGTAA
 -----+-----+-----+-----+-----+ 60
 TCACTAGTACCACCGTCCCTCGGTACCTTTTATCTCTGGGTGGGCCAAGACCCAGACCATT
 b M V A G A M E N R D P P G S G S G N -
 TGAAGTCATAGAAGGCCCCCAAATGCAAGAGTCTCTGAAGGGCTCCCAGGCTCGCTTCAA
 61 -----+-----+-----+-----+-----+ 120
 ACTTCAGTATCTTCCGGGGGTTTACGTTCTCAGGACTTCCCAGGGTCCGAGCGAAGTT
 b E V I E G P Q N A R V L K G S Q A R F N -
 CTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCT
 121 -----+-----+-----+-----+-----+ 180
 GACGTGGCAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGTACCACCACGA
 b C T V S Q G W K L I M W A L S D M V V L -
 AAGCGTCAGGCCCATGGAGCCCATCATCACCATGACCGCTTCACCTCTCAGAGGTACGA
 181 -----+-----+-----+-----+-----+ 240
 TTCGCAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCGAAGTGGAGAGTCTCCATGCT
 b S V R P M E P I I T N D R F T S Q R Y D -
 CCAGGGCGGGAACCTTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTCGGG
 241 -----+-----+-----+-----+-----+ 300
 GGTCCCGCCCTTGAAGTGGAGCCTCTACTAGTAGGTGTACACCTCGGGTCACTAAGCCC
 b Q G G N F T S E M I I H N V E P S D S G -
 GAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCA
 301 -----+-----+-----+-----+-----+ 360
 CTTGTAGTCTACGTCGGAGGTCTTGTGACGGACGTACCTAGACGAATGGAATGGCAGGT
 b N I R C S L Q N S R L H G S A Y L T V Q -
 AGTTATGGGAGAGCTGTTTCAATCCAGTGTTAATCTTGTAGTCGCTGAGAATGAACCTTG
 361 -----+-----+-----+-----+-----+ 420
 TCAATACCCTCTCGACAAGTAAGGGTCACAATTAGAACATCAGCGACTCTTACTTGAAC
 b V M G E L F I P S V N L V V A E N E P C -
 TGAAGTTACTTGTCTACCCTCACACTGGACCTGGCTCCCGGATATTTCTGGGAGCTCGG
 421 -----+-----+-----+-----+-----+ 480
 ACTTCAATGAACAGATGGGAGTGTGACCTGGACCGAGGGCCTATAAAGGACCCTCGAGCC
 b E V T C L P S H W T W L P D I S W E L G -
 TCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCGGAGCCCAGCGACCTTCAAAGTGC
 481 -----+-----+-----+-----+-----+ 540
 AGAGGACCAGTCGGTAAGTTTCGATAATAAAACAAGGCCTCGGGTCGCTGGAAGTTTCACG
 b L L V S H S S Y Y F V P E P S D L Q S A -
 AGTGAGCATCCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTGCGTGGCTACCTG
 541 -----+-----+-----+-----+-----+ 600
 TCACTCGTAGGACCGAGACTGGGGTGTCTCGTTACCCTGAAACTGAACGCACCGATGGAC
 b V S I L A L T P Q S N G T L T C V A T W -

FIGURE 2 (con't)

601 GAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTCCGGTGTCCCCA
 -----+-----+-----+-----+-----+ 660
 CTTCTCGGACTTCCGGGCGTTTCAGACGTTGACATTAGAGTGACACTAAGCCACAGGGGT
 b K S L K A R K S A T V N L T V I R C P Q -
 661 AGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTAGGTTT
 -----+-----+-----+-----+-----+ 720
 TCTGTGACCTCCACCATAATTATAAGGTCCACATAATAGTTCAAATGGCTCAAATCCAAA
 b D T G G G I N I P G V L S S L P S L G F -
 721 TTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCC
 -----+-----+-----+-----+-----+ 780
 AAGTAACGGATGAACCCCGTTTCAACCTGAACCTGATCGTCCGTGGTACGAAGACTGCGG
 b S L P T W G K V G L G L A G T M L L T P -
 781 GACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTG
 -----+-----+-----+-----+-----+ 840
 CTGCACATGAGAATGTTATGCGACGACGACGCGCGGCAGCAACAACACCGACGTTGAC
 b T C T L T I R C C C C R R R C C G C N C -
 841 CTGCTGCCGTTGTTGTTTCTGCTGTAGAAGAAAAAGAGGATTTTCGTATTCAATTTCAAAA
 -----+-----+-----+-----+-----+ 900
 GACGACGGCAACAACAAAGACGACATCTTCTTTTCTCCTAAAGCATAAGTTAAAGTTT
 b C C R C C F C C R R K R G F R I Q F Q K -
 901 GAAATCTGAAAAAGAGAAGACAAACAAAGAACTGAGACAGAAAGTGGAAATGAAACTC
 -----+-----+-----+-----+-----+ 960
 CTTTAGACTTTTTCTCTTCTGTTTGTCTTTGACTCTGTCTTTACCTTTACTTTTGAG
 b K S E K E K T N K E T E T E S G N E N S -
 961 CGGCTACAATTCAGATGAACAAAAGACCACAGACACCGCTTCTCTCCCTCCCAAATCCTG
 -----+-----+-----+-----+-----+ 1020
 GCCGATGTTAAGTCTACTTGTCTTCTGTTGTTCTGTGGCGAAGAGAGGGAGGTTTAGGAC
 b G Y N S D E Q K T T D T A S L P P K S C -
 1021 TGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCCTCACCAGCGGGCTGA
 -----+-----+-----+-----+-----+ 1080
 ACTTAGGTCACTAGGACTTGTCTTCTTGTGTCATCGACACCGGGAGGAGTGGTCGCCCCGACT
 b E S S D P E Q R N S S C G P P H Q R A D -
 1081 TCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCTGGCCAGTCCTGA
 -----+-----+-----+-----+-----+ 1140
 AGTTGCAGGTGGGTCCGGTTCAGTAGGTGTCCGAAGAAAATTAGACCGGTCAGGACT
 b Q R P P R P A S H P Q A S F N L A S P E -
 1141 GAAGGTCAGTAATACAACCTGTAGTATAG
 -----+-----+-----+-----+ 1168
 CTTCCAGTCATTATGTTGACATCATATC
 b K V S N T T V V * -

FIGURE 3

1 AGGTGTGAGTCCAGCCAACAGTGTGGATCAGTTTCCTAGGCTGCCATAACAAAGCACCAT
 -----+-----+-----+-----+-----+-----+ 60
 TCCACACTCAGGTCGGTTGTACACCTAGTCAAAGGATCCGACGGTATTGTTTCGTGGTA

61 AACCTGGTGGCTTAGAACAATGGAAAGGCATTTGCTCACGGTTCCAGAAGCTGTAGGTTT
 -----+-----+-----+-----+-----+-----+ 120
 TTGGACCACCGAATCTTGTACCTTTCCGTAAACGAGTGCCAAGGTCTTCGACATCCAAG

b M E R H L L T V P E A V G S -

121 TGGGTCTGGTAATGAAGTCATAGAAGGCCCCAGAAATGCAACAGTCCTGAAGGGCTCCCA
 -----+-----+-----+-----+-----+-----+ 180
 ACCCAGACCATTACTTCAGTATCTTCCGGGGGTCTTACGTTGTGAGGACTTCCCGAGGGT

b G S G N E V I E G P Q N A T V L K G S Q -

181 GGCTCGCTTCAACTGCACCGTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGA
 -----+-----+-----+-----+-----+-----+ 240
 CCGAGCGAAGTTGACGTGGCAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACT

b A R F N C T V S Q G W K L I M W A L S D -

241 CATGGTGGTGTCTAAGCGTCAGGCCCATGGAGCCCATCATCACCATGACCGCTTCACCTC
 -----+-----+-----+-----+-----+-----+ 300
 GTACCACCACGATTTCGAGTCCGGGTACCTCGGGTAGTAGTGGTTACTGGCGAAGTGGAG

b M V V L S V R P M E P I I T N D R F T S -

301 TCAGAGGTACGACCAGGGCGGGAACCTTCACCTCGGAGATGATCATCCACAATGTGGAGCC
 -----+-----+-----+-----+-----+-----+ 360
 AGTCTCCATGCTGGTCCCCGCCCTTGAAGTGGAGCCTCTACTAGTAGGTGTTACACCTCGG

b Q R Y D Q G G N F T S E M I I H N V E P -

361 CAGTGATTGGGGGAACATCAGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTA
 -----+-----+-----+-----+-----+-----+ 420
 GTCACTAAGCCCCCTGTAGTCTACGTCGGAGGTCTTGTGAGCGGACGTACCTAGACGAAT

b S D S G N I R C S L Q N S R L H G S A Y -

421 CCTTACCGTCCAAGTTATGGGAGAGCTGTTTCATTCCTCAGTGTTAATCTTGTAGTCGCTGA
 -----+-----+-----+-----+-----+-----+ 480
 GGAATGGCAGGTTCAATACCCCTCTCGACAAGTAAGGGTCACAATTAGAACATCAGCGACT

b L T V Q V M G E L F I P S V N L V V A E -

481 GAATGAACCTTGTGAAGTTACTTGTCTACCTCACACTGGACCCGGCTCCCGGATATTTT
 -----+-----+-----+-----+-----+-----+ 540
 CTTACTTGGAACACTTCAATGAACAGATGGGAGTGTGACCTGGGCCGAGGGCCTATAAAG

b N E P C E V T C L P S H W T R L P D I S -

541 CTGGGAGCTCGGTCTCCTGGTCAGCCATTCAAGCTATTATTTTGTTCGGAGCCCAGCGA
 -----+-----+-----+-----+-----+-----+ 600
 GACCTCGAGCCAGAGGACAGTCGGTAAGTTCGATAATAAAACAAGGCTCGGGTCGCT

b W E L G L L V S H S S Y Y F V P E P S D -

FIGURE 3 (con't)

1201 GGCCAGTCCTGAGAAGGTCAGTAATACAACCTGTAGTATAG
-----+-----+-----+-----+ 1240
CCGGTCAGGACTCTTCCAGTCATTATGTTGACATCATATC

b A S P E K V S N T T V V * -

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FIGURE 4

1 ATGGTGGCAGGAGCCATGGAAAATAGAGACCCACCGGTTCTGGGTCTGGTAATGAAGTC
 TACCACCGTCCTCGGTACCTTTTATCTCTGGGTGGGCCAAGACCCAGACCATTACTTCAG 60
 a M V A G A M E N R D P P G S G S G N E V -
 ATAGAAGGCCCCCAAATGCAAGAGTCCTGAAGGGCTCCAGGCTCGCTTCAACTGCACC
 61 TATCTTCCGGGGGTTTTACGTTCTCAGGACTTCCCGAGGGTCCGAGCGAAGTTGACGTGG 120
 a I E G P Q N A R V L K G S Q A R F N C T -
 GTCTCCCAGGGCTGGAAGCTCATCATGTGGGCTCTCAGTGACATGGTGGTGCCTAAGCGTC
 121 CAGAGGGTCCCGACCTTCGAGTAGTACACCCGAGAGTCACTGTACCACCACGATTTCGCAG 180
 a V S Q G W K L I M W A L S D M V V L S V -
 AGGCCCATGGAGCCCATCATCACCAATGACCGCTTCACCTCTCAGAGGTACGACCAGGGC
 181 TCCGGGTACCTCGGGTAGTAGTGGTTACTGGCGAAGTGGAGAGTCTCCATGCTGGTCCCG 240
 a R P M E P I I T N D R F T S Q R Y D Q G -
 GGAACCTCACCTCGGAGATGATCATCCACAATGTGGAGCCCAGTGATTGGGGGAACATC
 241 CCCTTGAGTGGAGCCTCTACTAGTAGGTGTACACCTCGGGTCACTAAGCCCCTTGTTAG 300
 a G N L T S E M I I H N V E P S D S G N I -
 AGATGCAGCCTCCAGAACAGTCGCCTGCATGGATCTGCTTACCTTACCGTCCAAGTTATG
 301 TCTACGTCGGAGGTCTTGTACAGCGGACGTACCTAGACGAATGGAATGGCAGGTTCAATAC 360
 a R C S L Q N S R L H G S A Y L T V Q V M -
 GGAGAGCTGTTTATTCCCAGTGTAACTTGTAGTCGCTGAGAATGAACCTTGTGAAGTT
 361 CCTCTCGACAAGTAAGGGTCACAATTAGAACATCAGCGACTCTTACTTGAACACTTCAA 420
 a G E L F I P S V N L V V A E N E P C E V -
 ACTTGTCTACCCTCACACTGGACCCGGCTCCCGGATATTTCTGGGAGCTCGGTCTCCTG
 421 TGAACAGATGGGAGTGTGACCTGGGCCGAGGGCCTATAAAGGACCCTCGAGCCAGAGGAC 480
 a T C L P S H W T R L P D I S W E L G L L -
 GTCAGCCATTCAAGCTATTATTTTGTTCGGGAGCCCAGCGACCTTCAAAGTGCAGTGAGC
 481 CAGTCGGTAAGTTCGATAATAAACAAGGCCTCGGGTCGCTGGAAGTTTACGTCACTCG 540
 a V S H S S Y Y F V P E P S D L Q S A V S -
 ATCCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTGCGTGGCTACCTGGAAGAGC
 541 TAGGACCGAGACTGGGGTGTCTCGTTACCTGAAACTGAACGCACCGATGGACCTTCTCG 600
 a I L A L T P Q S N G T L T C V A T W K S -

FIGURE 4 (con't)

601 CTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGATTCCGGTGTCCCCAAGACACT
 -----+-----+-----+-----+-----+ 660
 GACTTCCGGGCGTTCAGACGTTGACATTTAGAGTGACACTAAGCCACAGGGGTTCTGTGA
 a L K A R K S A T V N L T V I R C P Q D T -
 661 GGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACCGAGTTTATAGGTTTTTCATTG
 -----+-----+-----+-----+-----+ 720
 CCTCCACCATAATTATAAGGTCCACATAATAGTTCAAATGGCTCAAATCCAAAAGTAAC
 a G G G I N I P G V L S S L P S L G F S L -
 721 CCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCATGCTTCTGACGCCGACGTGT
 -----+-----+-----+-----+-----+ 780
 GGATGAACCCCGTTTCAACCTGAACCTGATCGTCCGTGGTACGAAGACTGCGGCTGCACA
 a P T W G K V G L G L A G T M L L T P T C -
 781 ACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCGTTGTTGTGGCTGCAACTGCTGCTGC
 -----+-----+-----+-----+-----+ 840
 TGAGAATGTTATGCGACGACGACGACGGCGGAGCAACAACACCGACGTTGACGACGACG
 a T L T I R C C C C R R R C C G C N C C C -
 841 CGTTGTTGTTTCTGCTGTAGAAGAAAAAGAGGAAATCTGAAAAAGAGAAGACAAACAAAG
 -----+-----+-----+-----+-----+ 900
 GCAACAACAAGACGACATCTTCTTTTCTCCTTTAGACTTTTCTCTTCTGTTTGTTC
 a R C C F C C R R K R G N L K K R R Q T K -
 901 AACTGAGACAGAAAGTGAAATGAAACTCCGGCTACAATTCAGATGAACAAAAGACCA
 -----+-----+-----+-----+-----+ 960
 TTTGACTCTGTCTTTCACCTTTACTTTTGAGGCCGATGTTAAGTCTACTTGTTCCTGTT
 a K L R Q K V E M K T P A T I Q M N K R P -
 961 CAGACACCGCTTCTCTCCCTCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACA
 -----+-----+-----+-----+-----+ 1020
 GTCTGTGGCGAAGAGAGGGAGGGTTTAGGACACTTAGGTCCTAGGACTTGTTCCTTTGT
 a Q T P L L S L P N P V N P V I L N K E T -
 1021 GTAGCTGTGGCCCTCCTCACCAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATC
 -----+-----+-----+-----+-----+ 1080
 CATCGACACCGGGAGGAGTGGTCGCCCCGACTAGTTGCAGGTGGGTCCGGTCGTTTCAGTAG
 a V A V A L L T S G L I N V H P G Q Q V I -
 1081 CACAGGCTTCTTTAATCTGGCCAGTCCTGAGAAGGTCAGTAATACAACCTGTAGTATAA
 -----+-----+-----+-----+-----+ 1139
 GTGTCCGAAGAAAATTAGACCGGTCAGGACTCTTCAGTCATTATGTTGACATCATATT
 a H R L L L I W P V L R R S V I Q L *

FIGURE 5

1 GTGAACGAGATACAGAGATTTACCTGCCTGAGGTAAGGAAGATCATGCTGAGATGGAGGG
 -----+-----+-----+-----+-----+-----+ 60
 CACTTGCTCTATGTCTCTAAATGGACGGACTCCATTCTCTAGTACGACTCTACCTCCC
 b M E G -
 CAGCTGGAGAGATGTCCTGGCTGTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATC
 61 -----+-----+-----+-----+-----+ 120
 GTCGACCTCTCTACAGGACCGACACGACCAGTAGGACCGAGTCGACTGTGCAAGGCCTAG
 b S W R D V L A V L V I L A Q L T A S G S -
 CAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCA
 121 -----+-----+-----+-----+-----+ 180
 GTCAATAGTCTAGTATCTTCCAGGAGTCTTACATTGTGTCAGGATTTCTCTGAGTCTCCGAGT
 b S Y Q I I E G P Q N V T V L K D S E A H -
 CTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGT
 181 -----+-----+-----+-----+-----+ 240
 GAAGTTGACGTGGCACTGAGTGCCGACCTTCAAGAGTACACCTGAGAATTGGTTTACCA
 b F N C T V T H G W K L L M W T L N Q M V -
 GGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTTCACCTATGCCAG
 241 -----+-----+-----+-----+-----+ 300
 CCACGACTCAGAGTGGTGGGTCTCGGTAGTAGTGGTTGTTGGCGAAGTGGATACGGTC
 b V L S L T T Q G P I I T N N R F T Y A S -
 TTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGA
 301 -----+-----+-----+-----+-----+ 360
 AATGTTGTCGTGACTGTGCAAGTAGAGCCTCAACTAGTAGGTACTACACGTCGGGTCACT
 b Y N S T D S F I S E L I I H D V Q P S D -
 CTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTC
 361 -----+-----+-----+-----+-----+ 420
 GAGCCCTAGGCACGTTACGTCGGACGTCTTGTCCGTACCCAAACCTAGACGGAAGGAGAG
 b S G S V Q C S L Q N S H G F G S A F L S -
 AGTGCAAGTCATGGGGACCCTGAACATTCCTAGCAACAACCTTATAGTCACTGAGGGTGA
 421 -----+-----+-----+-----+-----+ 480
 TCACGTTCACTACCCCTGGGACTTGTAAGGATCGTTGTTGGAATATCAGTGACTCCCACT
 b V Q V M G T L N I P S N N L I V T E G E -
 ACCCTGTAATGTGACTTGCTATGCCGTGGGCTGGACCTCACTCCCGGATATTTCTTGGA
 481 -----+-----+-----+-----+-----+ 540
 TGGGACATTACACTGAACGATACGGCACCCGACCTGGAGTGAGGGCCTATAAAGGACCT
 b P C N V T C Y A V G W T S L P D I S W E -
 GCTTGAGGTTCCCGTAAGCCATTCGAGTTACAATTCCTTTCTGGAGCCGGGCAACTTTAT
 541 -----+-----+-----+-----+-----+ 600
 CGAACTCCAAGGCATTCGGTAAGCTCAATGTTAAGGAAAGACCTCGGCCCCGTTGAAATA
 b L E V P V S H S S Y N S F L E P G N F M -

FIGURE 5 (con't)

601 GAGGGTCTTGAGTGTCTGACCTCACACCACTGGGCAACGGGACCTTGACTTGTGTGGC
 -----+-----+-----+-----+-----+ 660
 CTCCCAGAACTCACAGGACCTGGAGTGTGGTGACCCGTTGCCCTGGAAGTGAACACACCG
 b R V L S V L D L T P L G N G T L T C V A -
 661 AGAGCTGAAGGACTTGCAGGCCAGCAAGTCCTTAACTGTCAACCTGACTGTGGTTTCAGCC
 -----+-----+-----+-----+-----+ 720
 TCTCGACTTCCTGAACGTCCGGTCGTTTCAGGAATTGACAGTTGGACTGACACCAAGTCGG
 b E L K D L Q A S K S L T V N L T V V Q P -
 721 TCCACCTGACAGTATTGGAGAGGAAGGCCAGCACTGCCGACCTGGGCCATCATCCTGCT
 -----+-----+-----+-----+-----+ 780
 AGGTGGACTGTCATAACCTCTCCTTCCGGGTCGTGACGGCTGGACCCGGTAGTAGACGA
 b P P D S I G E E G P A L P T W A I I L L -
 781 GGCAGTGGCCTTTTCCTTGCTCTTGATCCTGATCATTTGTTTTGATTATAATATTCTGTTG
 -----+-----+-----+-----+-----+ 840
 CCGTCACCGGAAAAGGAACGAGAAGTAGGACTAGTAACAAAATAATATTATAAGACAAC
 b A V A F S L L L I L I I V L I I I F C C -
 841 CTGTTGTGCCTCCAGGAGAGAAAAGGAAGAATCTACTTATCAAAATGAAATAAGGAAATC
 -----+-----+-----+-----+-----+ 900
 GACAACACGGAGGTCCTCTCTTTCTCTTCTTAGATGAATAGTTTTACTTTATTCCTTTAG
 b C C A S R R E K E E S T Y Q N E I R K S -
 901 TGCAAACATGAGGACAAACAAAGCAGATCCGGAGACAAAGTAAAAAGTGGAAAGGAAAA
 -----+-----+-----+-----+-----+ 960
 ACGTTTGACTCCTGTTTGTTCGTCTAGGCCTCTGTTTCAATTTTTCACCTTTTCCTTTT
 b A N M R T N K A D P E T K L K S G K E N -
 961 CTACGGGTACAGTTCGGATGAGGCAAAGGCTGCACAGACTGCATCTCTCCCTCCTAAATC
 -----+-----+-----+-----+-----+ 1020
 GATGCCCATGTCAAGCCTACTCCGTTTCCGACGTGTCTGACGTAGAGAGGGAGGATTTAG
 b Y G Y S S D E A K A A Q T A S L P P K S -
 1021 TGCTGAAGTCAGCCTTCCAGAAAAACGCAGCAGTAGCCTTCTTATCAGGAAGTCAATAA
 -----+-----+-----+-----+-----+ 1080
 ACGACTTCAGTCGGAAGGTCTTTTTCGTCGTCATCGGAAGGAATAGTCCTTGAGTTATT
 b A E V S L P E K R S S S L P Y Q E L N K -
 1081 ACATCAGCCCGGTCCAGCAACTCATCCACGGGTTTCCTTTGACATCGCCAGTCCTCAGAA
 -----+-----+-----+-----+-----+ 1140
 TGTAGTCGGGCCAGGTCGTTGAGTAGGTGCCCAAAGGAACTGTAGCGGTCAGGAGTCTT
 b H Q P G P A T H P R V S F D I A S P Q K -
 1141 GGTCAGAAATGTGACTTTAGTGTAATAAAGACTTCTCATGACTGTACTTGGTGCA
 -----+-----+-----+-----+-----+ 1195
 CCAGTCTTTACTGAAATCACATTATTTCTGAAGAGTACTGACATGAACCACGT
 b V R N V T L V *

FIGURE 6

1 GTGAACGAGATACAGAGATTTACCTGCCTGAGGTAAGGAAGATCATGCTGAGATGGAGGG
 -----+-----+-----+-----+-----+-----+-----+ 60
 CACTTGCTCTATGTCTCTAAATGGACGGACTCCATTCCCTTCTAGTACGACTCTACCTCCC
 b M E G -
 61 CAGCTGGAGAGATGTCTTGGCTGTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATC
 -----+-----+-----+-----+-----+-----+ 120
 GTCGACCTCTCTACAGGACCGACACGACCAGTAGGACCGAGTCGACTGTCTGAAGGCCTAG
 b S W R D V L A V L V I L A Q L T A S G S -
 121 CAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCA
 -----+-----+-----+-----+-----+-----+ 180
 GTCAATAGTCTAGTATCTTCCAGGAGTCTTACATTGTCTAGGATTTCTGAGTCTCCGAGT
 b S Y Q I I E G P Q N V T V L K D S E A H -
 181 CTTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGT
 -----+-----+-----+-----+-----+-----+ 240
 GAAGTTGACGTGGCACTGAGTGCCGACCTTCAAGAGTACACCTGAGAATTGGTTTACCA
 b F N C T V T H G W K L L M W T L N Q M V -
 241 GGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCACAACCGCTTCACCTATGCCAG
 -----+-----+-----+-----+-----+-----+ 300
 CCACGACTCAGAGTGGTGGGTTCTGCGGTAGTAGTGGTTGGCGAAGTGGATACGGTC
 b V L S L T T Q G P I I T N N R F T Y A S -
 301 TTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGTGCAGCCAGTGA
 -----+-----+-----+-----+-----+-----+ 360
 AATGTTGTCGTGACTGTCTGAAGTAGAGCCTCAACTAGTAGGTACTACACGTCGGGTCACT
 b Y N S T D S F I S E L I I H D V Q P S D -
 361 CTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTC
 -----+-----+-----+-----+-----+-----+ 420
 GAGCCCTAGGCACGTTACGTGCGACGTCTTGTCTGGTACCCAAACCTAGACGGAAGGAGAG
 b S G S V Q C S L Q N S H G F G S A F L S -
 421 AGTGCAAGACAGTATTGGAGAGGAAGGCCAGCACTGCCGACCTGGGCCATCATCCTGCT
 -----+-----+-----+-----+-----+-----+ 480
 TCACGTTCTGTCATAACCTCTCCTTCCGGGTCGTGACGGCTGGACCCGGTAGTAGGACGA
 b V Q D S I G E E G P A L P T W A I I L L -
 481 GGCAGTGGCCTTTTCCTTGCTCTTGATCCTGATCATTGTTTTGATTATAATATTCTGTTG
 -----+-----+-----+-----+-----+-----+ 540
 CCGTCACCGGAAAAGGAACGAGAACTAGGACTAGTAACAAAATAATATTATAAGACAAC
 b A V A F S L L L I L I I V L I I I F C C -
 541 CTGTTGTGCCTCCAGGAGAGAAAAGGAAGAATCTACTTATCAAAATGAAATAAGGAAATC
 -----+-----+-----+-----+-----+-----+ 600
 GACAACACGGAGGTCCTCTCTTTTCCTTCTTAGATGAATAGTTTACTTTATTCCTTTAG
 b C C A S R R E K E E S T Y Q N E I R K S -
 601 TGCAAACATGAGGACAAACAAAGCAGATCCGGAGACAAAGTTAAAAAGTGAAAGGAAAA
 -----+-----+-----+-----+-----+-----+ 660
 ACGTTTGTACTCCTGTTTGTTCGTCTAGGCCTCTGTTTCAATTTTTCACCTTTCCTTTT
 b A N M R T N K A D P E T K L K S G K E N -

FIGURE 3 (con't)

601 CCTTCAAAGTGCAGTGAGCATCCTGGCTCTGACCCACAGAGCAATGGGACTTTGACTTG
 -----+-----+-----+-----+-----+ 660
 GGAAGTTTCACGTCACTCGTAGGACCGAGACTGGGGTGTCTCGTTACCCGTAAACTGAAC
 b L Q S A V S I L A L T P Q S N G T L T C -
 661 CGTGGCTACCTGGAAGAGCCTGAAGGCCCGCAAGTCTGCAACTGTAAATCTCACTGTGAT
 -----+-----+-----+-----+ 720
 GCACCGATGGACCTTCTCGGACTTCCGGGCGTTCAGACGTTGACATTTAGAGTGACACTA
 b V A T W K S L K A R K S A T V N L T V I -
 721 TCGGTGTCCCAAGACACTGGAGGTGGTATTAATATTCCAGGTGTATTATCAAGTTTACC
 -----+-----+-----+-----+ 780
 AGCCACAGGGGTCTGTGACCTCCACCATAATTATAAGGTCCACATAATAGTTCAAATGG
 b R C P Q D T G G G I N I P G V L S S L P -
 781 GAGTTTAGGTTTTTCATTGCCTACTTGGGGCAAAGTTGGACTTGGACTAGCAGGCACCAT
 -----+-----+-----+-----+ 840
 CTCAAATCCAAAAGTAACGGATGAACCCCGTTCAACCTGAACCTGATCGTCCGTGGTA
 b S L G F S L P T W G K V G L G L A G T M -
 841 GCTTCTGACGCCGACGTGTACTCTTACAATACGCTGCTGCTGCTGCCGCCGTCTGTTGTTG
 -----+-----+-----+-----+ 900
 CGAAGACTGCGGCTGCACATGAGAATGTTATGCGACGACGACGACGGCGGCAGCAACAAC
 b L L T P T C T L T I R C C C C R R R C C -
 901 TGGCTGCAACTGCTGCTGCCGTTGTTGTTTCTGCTGTAGAAGAAAAGAGGATTTTCGTAT
 -----+-----+-----+-----+ 960
 ACCGACGTTGACGACGACGGCAACAACAAGACGACATCTTCTTTTTCTCTAAAGCATA
 b G C N C C C R C C F C C R R K R G F R I -
 961 TCAATTTCAAAGAAATCTGAAAAAGAGAAGACAAACAAGAAACTGAGACAGAAAGTGG
 -----+-----+-----+-----+ 1020
 AGTTAAAGTTTTCTTTAGACTTTTTCTTCTGTTTGTCTTTGACTCTGTCTTTTACC
 b Q F Q K K S E K E K T N K E T E T E S G -
 1021 AAATGAAAACCTCCGGCTACAATTCAGATGAACAAAAGACCACAGAAACCGCTTCTCTCCC
 -----+-----+-----+-----+ 1080
 TTTACTTTTGAGGCCGATGTTAAGTCTACTTGTCTTTCTGGTGTCTTTGGCGAAGAGAGGG
 b N E N S G Y N S D E Q K T T E T A S L P -
 1081 TCCCAAATCCTGTGAATCCAGTGATCCTGAACAAAGAAACAGTAGCTGTGGCCCTCTCA
 -----+-----+-----+-----+ 1140
 AGGGTTTAGGACACTTAGGTCACTAGGACTTGTCTTTGTCTATCGACACCGGGAGGAGT
 b P K S C E S S D P E Q R N S S C G P P H -
 1141 CCAGCGGGCTGATCAACGTCCACCCAGGCCAGCAAGTCATCCACAGGCTTCTTTTAATCT
 -----+-----+-----+-----+ 1200
 GGTGCGCCGACTAGTTGCAGGTGGGTCCGGTTCAGTAGGTGTCCGAAGAAAATTAGA
 b Q R A D Q R P P R P A S H P Q A S F N L -

FIGURE 7

1 GTGAACGAGATACAGAGATTTACCTGCCTGAGGTAAGGAAGATCATGCTGAGATGGAGGG
 -----+-----+-----+-----+-----+-----+ 60
 CACTTGCTCTATGTCTCTAAATGGACGGACTCCATTCTTCTAGTACGACTCTACCTCCC
 b M E G -
 61 CAGCTGGAGAGATGTCCTGGCTGTGCTGGTCATCCTGGCTCAGCTGACAGCTTCCGGATC
 -----+-----+-----+-----+-----+ 120
 GTCGACCTCTCTACAGGACCGACACGACCAGTAGGACCGAGTCGACTGTGCAAGGCCTAG
 b S W R D V L A V L V I L A Q L T A S G S -
 121 CAGTTATCAGATCATAGAAGGTCCTCAGAATGTAACAGTCCTAAAGGACTCAGAGGCTCA
 -----+-----+-----+-----+-----+ 180
 GTCAATAGTCTAGTATCTTCCAGGAGTCTTACATTGTCTAGGATTTCTGAGTCTCCGAGT
 b S Y Q I I E G P Q N V T V L K D S E A H -
 181 CTCAACTGCACCGTGACTCACGGCTGGAAGCTTCTCATGTGGACTCTTAACCAAATGGT
 -----+-----+-----+-----+-----+ 240
 GAAGTTGACGTGGCACTGAGTGCCGACCTTCAAGAGTACACCTGAGAATTGGTTTACCA
 b F N C T V T H G W K L L M W T L N Q M V -
 241 GGTGCTGAGTCTCACCACCCAAGGACCCATCATCACCAACAACCGCTTCACCTATGCCAG
 -----+-----+-----+-----+-----+ 300
 CCACGACTCAGAGTGGTGGGTTCTTGGGTAGTAGTGGTTGTTGGCGAAGTGGATACGGTC
 b V L S L T T Q G P I I T N N R F T Y A S -
 301 TTACAACAGCACTGACAGCTTCATCTCGGAGTTGATCATCCATGATGTGCAGCCCAGTGA
 -----+-----+-----+-----+-----+ 360
 AATGTTGTCGTGACTGTGCAAGTAGAGCCTCAACTAGTAGGTACTACACGTCGGGTCACT
 b Y N S T D S F I S E L I I H D V Q P S D -
 361 CTCGGGATCCGTGCAATGCAGCCTGCAGAACAGCCATGGGTTTGGATCTGCCTTCCTCTC
 -----+-----+-----+-----+-----+ 420
 GAGCCCTAGGCACGTTACGTCCGACGTCTTGTCCGTACCCAAACCTAGACGGAAGGAGAG
 b S G S V Q C S L Q N S H G F G S A F L S -
 421 AGTGCAAGAATCTACTTATCAAAATGAAATAAGGAAATCTGCAAACATGAGGACAAACAA
 -----+-----+-----+-----+-----+ 480
 TCACGTTCTTAGATGAATAGTTTACTTTATTCCTTTAGACGTTTGTACTCCTGTTTGT
 b V Q E S T Y Q N E I R K S A N M R T N K -
 481 AGCAGATCCGGAGACAAAGTTAAAAAGTGAAAGGAAACTACGGGTACAGTTCGGATGA
 -----+-----+-----+-----+-----+ 540
 TCGTCTAGGCCTCTGTTTCAATTTTTACCTTTCTTTTGTATGCCCATGTCAAGCCTACT
 b A D P E T K L K S G K E N Y G Y S S D E -
 541 GGCAAAGGCTGCACAGACTGCATCTCTCCCTCCTAAATCTGCTGAAGTCAGCCTTCCAGA
 -----+-----+-----+-----+-----+ 600
 CCGTTTCCGACGTGTCTGACGTAGAGAGGGAGGATTTAGACGACTTCAGTCGGAAGGTCT
 b A K A A Q T A S L P P K S A E V S L P E -



b K R S S S L P Y Q E L N K H Q P G P A T -

b H P R V S F D I A S P Q K V R N V T L V -

b *

*

FIGURE 8

1MEGSWRDVLAVLVILAQLTASGSSYQIIEGPQ 32
 1 MAYSCQPLQESPLLGFPRLRFIHLFVL.LLVGLLQI.SSGIVGQVSKSVR 48
 33 NVTVLKDSEAHFNCTVTHGWKLLMWTNLQMVVLSLTTQGPPII...TNNRF 79
 49 EKALL.SCDYKF.CSEEQSIHRIYWQKHDKMVLVSVISGVPEVWPVKYKNRT 96
 80 TYASYNSTDSEFISELIIHDVQPSDSGSGVQCSLQNSHGFGSAFL....SVQ 125
 97 VYDIANNYSFSLGLIL.....SDRGTYTCVVQRYEG.GSYVVKHLTTVE 140
 126 VMGTNLNIPSNLIVTEGEPC....NVTCYAVGWTSPLDISWELEVPVSHS 171
 141 LSVRADFPTPN.ITEYGNPSADIKRITCFASGGFPKPRLSW.LENGRELN 188
 172 SYNSFL..EP.GNFMVLSVLDLTPLGNGTLTCVAELKDLQASKSLTVNL 218
 189 GINTTISQDPESELYTISSQLDFNATYDHFIDCFIEYGDHVSQ....NF 234
 219 TVVQPPPDSEEGEPALPTW.....AIIILLAVAFSLLLILIIIVLIIF 261
 235 TWVKPPEDPPDEKQTVPFAGPDAVKAIIFFIATVIAVIAAIAIIF 284
 262 CCCCASRR.EKEESTYQNEIRKSANMRTNKADPETKLKSGKENYGYSSDE 310
 285 CITVKFRRCFRRRNEASRETNKNLYIGPVEAAAEQTV..... 321

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